

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 11, 2003, 02:05:38 ; Search time 37 Seconds
(without alignments)
280.609 Million cell updates/sec

Title: US-09-914-324A-1

Perfect score: 616
Sequence: 1 MAAMADVDPSTGNSGAGK.....KTRQVCPDLDNREMEFQKYGH 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	108	T51146	ring-box protein 1
2	510	82.8	136	T13388	hypothetical prote
3	499	81.0	115	T47341	ring-box protein-1
4	493	80.0	110	T27823	hypothetical prote
5	469	76.1	107	T38310	pop-interacting pr
6	385	62.5	121	S66830	hypothetical prote
7	378	61.4	166	T18513	hypothetical prote
8	266	43.2	112	T29620	hypothetical prote
9	164.5	26.7	94	T38652	hypothetical prote
10	146.5	23.8	135	T21802	hypothetical prote
11	136	22.1	165	S52511	hypothetical prote
12	132.5	21.5	99	G90113	Rbpl protein [limp
13	116.5	18.9	2160	T20241	hypothetical prote
14	104	16.9	349	T06680	hypothetical prote
15	102.5	16.6	249	C96775	probable RING zinc
16	102	16.6	210	T45634	zinc-finger-like p
17	100	16.2	676	T47637	hypothetical prote
18	97	15.7	159	T48209	hypothetical prote
19	97	15.7	327	D86474	probable RING zinc
20	96	15.6	332	E86448	hypothetical prote
21	95.5	15.5	441	T71425	hypothetical prote
22	95	15.4	253	T06113	hypothetical prote
23	95	15.4	322	H85474	hypothetical prote
24	95	15.4	336	T28358	ORF MSV197 tryptop
25	95	15.4	362	T51464	RING-H2 zinc-finge
26	95	15.4	530	T50499	hypothetical prote
27	95	15.4	689	E84811	probable retroelem
28	92	14.9	185	T51844	RING-H2 finger pro
29	91.5	14.9	190	T51859	RING-H2 finger pro

30	91.5	14.9	496	B96674	hypothetical prote
31	91.5	14.9	571	T40911	probable PHD-type
32	91	14.8	530	T28366	ORF MSV205 tryptop
33	90.5	14.7	677	T39713	zinc finger protei
34	90	14.6	213	T14811	hypothetical prote
35	90	14.6	532	T49467	hypothetical prote
36	89.5	14.5	1208	T05077	related to COP1-in
37	89.5	14.5	202	T06621	hypothetical prote
38	89.5	14.5	624	T01585	hypothetical prote
39	89	14.4	357	E85092	probable RING zinc
40	89	14.4	456	T19377	hypothetical prote
41	88.5	14.4	336	A86406	hypothetical prote
42	88.5	14.4	524	F96572	probable RING zinc
43	88	14.3	141	S15788	protein R12M16.10
44	88	14.3	161	E88541	intermediate early
45	88	14.3	200	T41745	protein ZK637.14 [
					RING-H2 finger pro

ALIGNMENTS

RESULT 1

T51146

ring-box protein 1 [imported] - human

C.Species: Homo sapiens (man)

C.Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000

C.Accession: T51146

R.Kamura, T.; Keop, D.M.; Conrad, M.N.; Skowrya, D.; Moreland, R.J.; Iliopoulos, O.;

Science 284, 657-661, 1999

A.Title: Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase

A.Reference number: 225317; PMID:99234320; PMID:10213691

A.Accession: T51146

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-108 <KAM>

A.Cross-references: EMBL:AF140598; PIDN:AAD29715.1

C.Genetics:

A.Gene: RBX1

Query Match

Best local similarity 100.0%; Score 616; DB 2; Length 108;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMADVDPSTGNSGAGKREVKKNVAVLAWMDIVVNDCAICRNHMDICIQANO 60

DB 1 MAAMADVDPSTGNSGAGKREVKKNVAVLAWMDIVVNDCAICRNHMDICIQANO 60

QY 61 ASATSECTVAVGVCNHAFFHCISRMLKTRQVCPDLDNREMEFQKYGH 108

DB 61 ASATSECTVAVGVCNHAFFHCISRMLKTRQVCPDLDNREMEFQKYGH 108

RESULT 2

T13388

hypothetical protein 11502.11 - fruit fly (Drosophila melanogaster)

C.Species: Drosophila melanogaster

C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

R.Salles, C.; Valenti, P.; Darlamiou, A.; Henderson, N.; Campbell, L.; Glover, D.

submitted to the EMBL Data Library, May 1999

A.Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A.Reference number: 217665

A.Accession: T13388

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-136 <CAT>

A.Cross-references: EMBL:AL031581; PIDN:CAA20888.1

C.Genetics:

A.Cross-references: FlyBase:FBgn0020381

A.Introns: 64/1

A.Note: EG:11502.11

Query Match

82.8%; Score 510; DB 2; Length 136;

Best Local Similarity	69.3%	Pred. No.	4e-47;
Matches	95;	Conservative	4;
		Mismatches	4;
		Indels	34;
		Gaps	3;

Best Local Similarity 79.38; Pred. No. 2.1e-45;
Matches 88; Conservative 5; Mismatches 14; Indels, 4; Gaps 2

[illegible]

RESULT 3
T47341
ring-box protein-like - Arabidopsis thaliana

N:Alternate names: protein T2IC14.50
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Aug-2002
C:Accession: T47341
R:Delseny, M.; Berger, C.; Cooke, R.; Gaubier, P.; Grellet, F.; Laudie, M.

submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24462

A:Accession: T47741
A:Status: preliminary
A:Molecule type: DNA
A:Residue: 1115 <DEI>
A:Cross-references: EMBL:AL138639
A:Experimental source: cultivar Columbia; BAC clone T21C14
A:Genetics:

C;Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match	81.0%	Score	499	DB	2	Length	115
Best Local Similarity	81.5%	Pred. NO.	5e-46				
Matches	88	Conservative	5	Mismatches	13	Indels	2
						Gaps	1

[illegible]

RESULT 4
T27823
hypothetical protein ZK287.5 - *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27823

submitted to the EMBL Data Library, April 1996
A:Reference number: Z20425

A:Accession: J27823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-110 <WILL>
A:Cross-references: EMBL:Z70757; PIDB:CAA94801.1; GSPDB:GN00023; CESP:ZK287.5
A:Experimental source: clone ZK287

A;Gene: CESP:ZK287.5
A;Map position: 5
A;Introns: 25/3; 94/3

Query Match	80.0%; Score 493; DB 2; Length 110;
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Oy 1 MAAMM---VDTPSGNSGAGKKREYKMYNVALMAMDIYDNCALCRHINDLCEG 57
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 1 MAQSDSTAEVEBEATNQTV-KKRFVKKMSVALMAMDIYDNCALCRHINDLCEG 59
    .
Oy 58 ANQASATSECTGANGVCNNAHNFHCISWYKTRVCGLDREKEPQYKH 108
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 60 ANQASGLKDECTYAGNCGNNAHNFHCISWYKTRVCGLDREKEPQYKH 110
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 5
T38310
pop-interacting protein 1 - fission yeast (*Schizosaccharomyces pombe*)
E. coli: Schizosaccharomyces pombe

C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_rev10n 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38310
R:Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, September 1997
A:Reference number: Z21733
Accession number: Z21733

A:accession: T38310
A:status: preliminary; translated from GB/EMBL/DBJ
A:molecule type: DNA
A:features: 1107 ntos

A:Residues: 1-107

A:Cross-references: EMBL:Z98977; PID:CA58559.1; GSPDB:GN00066; SPDB:SPAC23H4.18C
A:Experimental source: strain 972h; cosmid C23H4
C:Genetics:
A:Gene: SPDB:SPAC23H4.18C

Query Match	76.1%	Score 469	DB 2	length 107
Best Local Similarity	87.5%	Pred. No. 7.3e-43		
Matches 77	Conservative 4	Mismatches 7	Indels 0	Gaps 0

QY	21	REFEKKNNAAALAMPIIVYDNCALICRNHIMDICECOANASATSECTYAVWCJHAAH	80
Db	20	REFEKKNNAAALAMPIIVYDNCALICRNHIMDICECANIDMSAAQCTYAVNCTCHAAH	79
QY	81	FHCISRLKTRQVCPIDNENEFORXGH	108
Db	80	FHCISRLNTRVCPIDNENEFORIGH	107

RESULT
S66830

hypothetical protein YOL133w - yeast (*Saccharomyces cerevisiae*)

C:Species: *Saccharomyces cerevisiae*

C;Accession: S66830; S72035

submitted to the Protein Sequence Database, July 1996

A: Accession: S66830

A:Residues: 1-121 <ARI>
A:Cross-references: EMBL:Z74876; NID:g1420022; PID:g1420024; MIPS:YOL133w

R;Aldea, M.; Piedrafita, L.; Casas, C.; Casamayor, A.; Khalid, H.; Balcells, L.; Arin

A: Title: Sequence analysis of a 12 801 bp fragment of the left arm of yeast chromosome protein and six other open reading frames.

A;Reference number: S72030; MUID:97051593; PMID:8896270
A;Accession: S72035
A;Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-121 <AID>
A:Cross-references: EMBL:X95465; NID:g1628437; PIDN:CAA673.1; PID:g1628443
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, DNA
C:Genetics:
A:Gene: SGD:HRT1

A:Cross-references: SGD:S0005493
A:Map position: 15L
A:Note: YOL133w
C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 62.5%; Score 385; DB 2; Length 121;
Best Local Similarity 56.6%; Pred. No. 7.2e-34;
Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;
OY 5 MDVDTPSGTNSGAG-----KKRFVKKMAVALMAMDIYVNCALICRNHIMDL 54
DB 8 MDVDEDSQNTLAQSSNOSAPVETKKRFRKKTVAEWSMDIADVNCALICRNHIMEPCI 67
OY 55 ECGAQAASATSECTVAMGVCNHAFFHCISRWLKTQVCPDNRMEFEOKYG 107
DB 68 ECGPAMDTDNECVAMGVCNHAFFHCISRWLKTQVCPDNRMEFEOKYG 120

RESULT 7
T18513
hypothetical protein C0845c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T18513
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z18935
A:Accession: T18513
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <LAW>
A:Cross-references: EMBL:Z98551; PIDN:CA11123.2
C:Genetics:
A:Map position: 3
A:Introns: 19/1
A:Note: C0845c

Query Match 61.4%; Score 378; DB 2; Length 166;
Best Local Similarity 69.6%; Pred. No. 5.5e-33;
Matches 64; Conservative 5; Mismatches 15; Indels 8; Gaps 1;
OY 22 FEVKKMAVALMAMDIYVNCALICRNHIMDLCTECCO-----NQASATSECTVAMG 73
DB 72 FKIHWSAVAAMSWDICSVDNCAICRNHIMDLCTECCOAKTTDENDKDKIDREGCTVAMG 131
OY 74 VCNHAFHFCISRWLKTQVCPDNRMEFEOK 105
DB 132 VCNHAFHFCISRWLKTQVCPDNRMEFEOK 163

RESULT 8
T29620
hypothetical protein R10A10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
C:Accession: T29620
R:Wamsley, P.; Bradshaw, H.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid R10A10.
A:Reference number: Z20553
A:Accession: T29620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-112 <WAM>
A:Cross-references: EMBL:U80449; PIDN:AA837826.1; GSPDB:GN00019; CESP:R10A10.2
A:Experimental source: strain Bristol N2; clone R10A10
C:Genetics:
A:Gene: CESP:R10A10.2
A:Map position: 1
A:Introns: 17/2; 59/1
C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 43.2%; Score 266; DB 2; Length 112;

Best Local Similarity 41.3%; Pred. No. 3.1e-21;
Matches 45; Conservative 20; Mismatches 32; Indels 12; Gaps 2;

OY 1 MAAMVDTPSGTNSGAGKKR-----FEVKKMAVALMAMDIYVNCALICRNHIMDL 52
DB 1 MNNSVADQESSTSAQOKRTANPSESRRPVFLKMAVALMAMDVCDICATCRVHLMEE 60
OY 53 CTECQAASATSECTVAMGVCNHAFFHCISRWLKTQVCPDNRMEFEOKYG 101
DB 61 CLRCQ-----SEPSAECTVYMGDCNHSFHCICMTQWIRQNNRCPDCKQDW 105

RESULT 9
T38652
hypothetical protein SPAC343.03 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38652
R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21804
A:Accession: T38652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-94 <MUR>
A:Cross-references: EMBL:AL109739; NID:el534774; PIDN:CAB52266.1; GSPDB:GN00066; SPDB
A:Experimental source: strain 97zh-; cosmid c43
C:Genetics:
A:Gene: SPDB:SPAC343.03
A:Map position: 1
A:Introns: 7/1; 48/1

Query Match 26.7%; Score 164.5; DB 2; Length 94;
Best Local Similarity 33.7%; Pred. No. 1.7e-10;
Matches 28; Conservative 16; Mismatches 30; Indels 9; Gaps 3;

OY 21 REEVKKMAVALMAMDIYVNCALICRNHIMDLCTECCOQAASATSECTVAMGVCNHAFF 79
DB 2 KYKILMYHAIAMWTWTPKDDVGCICRVFDDGCCPGC-----TSPDNCPIVWKKCKHIF 56
OY 80 HFGCISRWLKT--ROYCPDNR 99
DB 57 HAVCIQNLATLSGSGCGCEPMDRQ 79

RESULT 10
T21802
hypothetical protein F35G12.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
C:Accession: T21802
R:Chui, C.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19473
A:Accession: T21802
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-135 <WIL>
A:Cross-references: EMBL:Z46242; PIDN:CA86328.1; GSPDB:GN00021; CESP:F35G12.9
A:Experimental source: clone F35G12
C:Genetics:
A:Gene: CESP:F35G12.9
A:Map position: 3
A:Introns: 33/3; 57/3
C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 23.8%; Score 146.5; DB 2; Length 135;
Best Local Similarity 33.3%; Pred. No. 2e-08;
Matches 28; Conservative 10; Mismatches 35; Indels 11; Gaps 3;
OY 24 VKKMAVALMAMDIYVNCALICRNHIMDLCTECCQAASATSECTVAMGVCNHAFFH 82

